



# FIG. 1A

(1:5, HEAVY CHAIN) [SEQ ID NO.: 1]

CDR1  
VQLLEQSGA EVRKPGSSVK VCKASGGTF SGHVIITWVRQ AFGQGLEWMG ESPIEGSAN YAONYAOKER DRVSIADTS TSTSFIELSN LRSDDTAVY CARDPPEYCS AGRCYTGFEQ QWGGQTLVTV SS

CDR2

CDR3

CDR1  
EVQLLEQSGA EVKKPGSSVK VSCQVFGDTF SRYTIQWLRLQ APGQGPFWMG NIIPVNTPN YAOKEQGRLS ITADDSTSTA YMESSLRSE DTAVYFCARV YIPNAIRHTM GYVEDIWWGG TILVTVSS

CDR2

CDR3

(1:7, HEAVY CHAIN) [SEQ ID NO.: 2]

# FIG. 1B



## FIG. 1C

(1:11, HEAVY CHAIN) [SEQ ID NO.: 3]

EVQLLEQSGA EVKKPGSSVK VSCKASGGTF SGHVSIVYRQ APQGILEWMG GSISEFGTSNLSAOKEDGRVS ITADESASTA YMEISSLRSE DTAIYYCAKD PPRECSGGINC YPGFEQOWGQ GTLVTYSS  
CDR1 CDR2 CDR3

EVQLLESGG WQPGRSRL SCAASGFTFK TYGMHWVRQA PGKGLEWVAG ISFDGSSNOYY ADSYKGRFV SRDNSRDTVF LQMSSLRLED TAVYYCATEG SPECSIKGRY YLENWGQGTL VTSS  
CDR1 CDR2 CDR3

(L3, HEAVY CHAIN) [SEQ ID NO.: 4]

## FIG. 1D



FIGURE 1E (L1, HEAVY CHAIN) [SEQ ID NO.: 5 ]

VQLLESGGG VQPGRLRL SCAASGFTFS <sup>CDR 1</sup>AYGMHWVRQA PGKGLEWVAG <sup>CDR 2</sup>IWFDGSGNQYYSDSVKGRFTV -  
<sup>CDR 3</sup>SRDNRNTLF LQMNSLRPED TAVYYCATEV LEGSIKGRYYLENWGGQGLTVTVSS

FIGURE 1F (A8, HEAVY CHAIN) [SEQ ID NO.: 6 ]

VQLLESGPG LVKPSGTL<sup>CDR 1</sup>SL TCTVSGGSIR SSHWWSWVRQ <sup>CDR 2</sup>PPGKGLEWIG EVFESGSTIYNPSLNDRVFM -  
<sup>CDR 3</sup>SVDKSKDQVS LRLSSVTAAD TAVYYCARSP IKMNQGRMMLDAFDIWGGQGLTVIVSS

FIGURE 1G (A12, HEAVY CHAIN) [SEQ ID NO.: 7 ]

VQLLESGSE VKKPGSSVKV SCRASGGSFR <sup>CDR 1</sup>SYNFENWVRQA PGQGLEWMGG <sup>CDR 2</sup>IIPMEGTANYAQKEQGRVTI -  
<sup>CDR 3</sup>TADESTATGY MELSSLRSED TAVYYCAMPY PKHCSRGSCW GWEDPWGGQGLTVTVSS



## FIG. 2A

(1:5, HEAVY CHAIN) [SEQ ID NO.: 8]

CDR1  
AELTQSPGTL SLSPGERATL SCRASQSVNK NYLAWYQQRP GOAPRLIIYG ASSRATGIPD RFSGSGSGTD FTLTISRLEP EDFAVYYCOL YGNRRTWTFGQ GTKVEIK  
CDR2  
CDR3

CDR1  
AELTQSPATL SLSPGERATL SCRASQSVNK YLAWYQQKPG QAPRLIIYDA SNRATGIPAR FSGSGSGTDF TLTISNLEPE DFAVYYCQOR SDWVITFGGGT KVEIK  
CDR2  
CDR3

(1:7, HEAVY CHAIN) [SEQ ID NO.: 9]

## FIG. 2B



FIG. 2C

(1:11, HEAVY CHAIN) [SEQ ID NO.: 10]

CDR1  
ELTQSPGTL SLSPGERATL SCGASQSVRS NYLAWYQQKP GQAPRLIYG VSSRATGIPD RFGSGSGTD FTLTISRLEP EDFAVYCCQ YGSSPRITFGQ GTKLEIK CDR3

CDR 1  
AELTQSPATL SVSPGERASL SCRASQSVGN NLAWYQQKP GQAPRLIYG NIRAIGTPDR FSGSGSGTEF ILTISSQSE DFAVYFCQHY STWPLTFGGG TKVEFK CDR3

(L3, HEAVY CHAIN) [SEQ ID NO.: 11]

FIG. 2D



FIGURE 2E (L1, LIGHT CHAIN) [SEQ ID NO.: 12 ]

ELTQSPGTL SLSVGERATL SCRASQNIYS GYLGWYQQKP GQPPRLIYG ASNRAIGIPD  
CDR 1 CDR 2

- RFSGSGSGTD FTLTISRLES EDFAVYCCQ YGSPPYTFGQ GTKVEIK  
CDR 3

FIGURE 2F (A8, LIGHT CHAIN) [SEQ ID NO.: 13 ]

ELTQSPSSL SAFVGDRVTI TCRASQSISR NLNWYQQKPG TAPKVLIIAA SSLQSGVPSR  
CDR 1 CDR 2

- FSGSGSGTDF TLTITSLQPE DFATYCCQS YTIPRIFGQG TKVEIK  
CDR 3

FIGURE 2G (A12, LIGHT CHAIN) [SEQ ID NO.: 14 ]

ELTQSPGTL SLSVGERATL SCRASQSLSS KYLAWYQQKP GQAPRIFIYD ASSRAIGIPD  
CDR 1 CDR 2 CDR 3

- RFSGSGSGTD FTLTISRLEP EDFAVYCCQ YGIPRIFGQG TKVEIK



## FIG. 3A

(1:5, HEAVY CHAIN) [SEQ ID NO.:15]

GAGCTCACGC AGTCTCCAGG CACCCTGTCT TTGTCTCCAG GGGAAGAGC CACCCTCTCC TGCAGGGCCA  
GTCAGAGTGT TAGCAGCAAT TACTTAGCCT GTACCAGCA GAGACCTGGC CAGGCTCCCA GGCTCCTCAT  
CTATGGTGCA TCCAGCAGGG CCACTGGCAT CCCAGACAGG TTCAGTGGCA GTGGTCTGG GACAGACTTC  
ACTCTACCA TCAGCAGACT GGAGCCTGAA GATTTGCGAG TGTATTACTG TCAGCTTTAT GGTAACCTCAC  
GTTGGACGTT CGGCCAAGG ACCAAGGTGG AGATCAAA

GAGTCACTC AGTCTCCAGC CACCCTGTCT TTGTCTCCAG GGGAAGAGC CACCCTCTCC TGCAGGGCCA  
GTCAGAGTGT TAACAAGTAC TTAGCCTGGT ACCAACAGAA ACCTGGCCAG GCTCCCAGGC TCCTCATCTA  
TGATGCATCC AACAGGGCCA CTGGCATCCC AGCCAGGTTT AGTGCCAGTG GGCTCTGGGAC AGACTTCACCT  
CTCACCATCA GCAACCTAGA GCCTGAAGAT TTTGCCAGTTT ATTACTGTCA GCAGCGTAGC GACTGGGTCA  
CTTTCGGCGG AGGGACCAAG GTGGAGATCA AA

(1:7, HEAVY CHAIN) [SEQ ID NO.: 16]

## FIG. 3B



## FIG. 3C

(1:11, HEAVY CHAIN) [SEQ ID NO.: 17]

GAGCTCACGC AGTCTCCAGG CACCCTGTCT TTGTCTCCAG GGAAGAGC CACCCTCTCC TCGGGGCCA  
GTCAGAGTGT TAGGAGCAAC TACTTAGCCT GGTACCAGCA AAAACCTGGC CAGGCTCCCA GGCTCCTCAT  
CTATGGTGT TCCAGCAGG CCACTGGCAT CCCAGACAGG TTCAGTGGCA GTGGTCTGG GACAGACTTC  
ACTCTACCA TCAGCAGACT GGAGCCTGAA GATTTGCG TGTATTACTG TCAGCAGTAT GGTAGCTCAC  
CTCGGACTTT TGGCCAGGG ACCAAGTTGG AGATCAAA

GAGCTCACGC AGTCTCCAGC CACCCTGTCT GTGTCTCCAG GGAAGAGC CTCCTCTCTCC TGCAGGGCCA  
GTCAGAGTGT CCGTAACAAT TTAGCTTGGT ATCAGCAGAA ACCTGGCCAG GCTCCCAGGC TCCTCATTTA  
TGGTGGAAC ACCAGAGCCA CTGGTACCCC AGACAGGTTT AGTGGCAGTG GGTCTGGGAC AGAATTCAC  
CTCACCATCA GCAGCCTGCA GTCTGAGGAC TTTGCAGTTT ATTCTGTCA AACTATAGT ACCTGGCCGC  
TCACCTTCGG CGGGGGACC AAGGTCGAGT TCAAG

(L3, HEAVY CHAIN) [SEQ ID NO.: 18]

## FIG. 3D





FIGURE 3E (L1, LIGHT CHAIN) [SEQ ID NO.: 19]

GAGGTGCAGC TGCTCGAGTC TGGGGGAGGC GTGGTCCAGC CTGGGAGGTC COTGAGACTC TCCTGTGCAG  
CGTCTGGATT CACCTTCAGT GCTTATGGCA TGCACCTGGT CCGCCAGGCT CCAGGCAAGG GGCTGGAGTG  
GGTGGCAGGT ATATGTTTG ATGGAAGTAA TCAATACTAT TCAGACTCCG TGAAGGGCCG ATTCACCGTC  
TCCAGAGACA ATCCAGGAA CAGGCTGTT CTGCAAAATGA ACAGCCTGAG ACCGAGGAC ACGGCTGTCT  
ATTACTGTGC GACAGAGGTA CTTTTGGAT CGATTAAAGG GCGTTACTAC CTTGAAAACT GGGGCCAGGG  
AACCCCTGGTC ACCGTCTCCT CA

FIGURE 3F (A8, LIGHT CHAIN) [SEQ ID NO.: 20]

GGGGAGCTCA CCCAGTCTCC ATCGTCCCTG TCTGCAATTG TNGGAGACAG AGTCACCATC ACTTGCCGGG  
CAAGTCAGAG TATTAGCAGG AACTTAAAT GGATCAGCA GAAACCCAGG ACAGCCCTA AGGTCTGTGAT  
CTATGCTGCA TCCAGTTTG AAGTGGGT CCCATCGAGG TTCAGTGGCA GTGATCTGG GACAGATTTC  
ACTCTCACC A TCACCACTCT GCAACCTGAA GATTTTGCA CTTACTATTG TCAACAGAGT TACACAACCC  
CTCGGACGTT CGGCCAAGG ACCAAGGTGG AAGTCAAA

FIGURE 3G (A12, LIGHT CHAIN) [SEQ ID NO.: 21]

GGCGAGCTCA CGCAGTCTCC AGGCACCCTG TCTTTGTCTC CAGGGGAAAG AGCCACCTC TCCTGCAGGG  
CCAGTCAGAG TCTTAGCAGC AAATACTTAG CNTGGTACCA ACAGAAOCT GGCCAGGCTC CCAGGCTCTT  
CATTTATGAT GCATCCAGCA GGGCCACTGG CATCCAGAC AGGTTCACTG GCAGTGGGTG TGGGACAGAC  
TTCACCTCTCA GCATCAGCAG ATTGGAGCCT GAAGATTTTG CAGTGATTA CTGTACAGCAG TATGGAACAC  
CTCGCACCTT CGGCCAGGG ACCAAGGTGG AAATCAAA

## FIG. 4A

(1:5, HEAVY CHAIN) [SEQ ID NO.: 22]

CTCGAGCAGT CTGGGGCTGA GGTGAGGAAG CCTGGGTCCT CGGTGAAGGT CTCCTGCAAG GCTTCTGGAG  
GCACCTTCAG CGGCCATGTT ATCACCTGGG TCGACAGGC CCTGGACAA GGACTTGAGT GGATGGGAGA  
GAGCATCCCT ATCTTTGGTT CCGCAAACTA CGCTCAAAAC TACGCTCAGA AATTCGGGA CAGAGTCTCG  
ATTATCGGG ACGAATCCAC GAGCACGTCTG TTCATTGAGC TGAGCAACCT GAGATCTGAC GACACGGCCG  
TCTACTACTG TCGGAGAGAC CCTCCAAGAT ATTGCAGTGC TGGTAGATGC TACCCGGGAT TCTTCCAGCA  
GTGGGGCCAG GGCACCCTCG TCACCCTCTC CTCA

CTCGAGCAGT CTGGGGCTGA GGTGAAGAAG CCTGGGTCCT CGGTGAAGGT CTCCTGTCAG GTTTTGGAG  
ACACCTTCAG CAGATACACT ATTCAGTGGT TCGACAGGC CCTGGACAA GGGCCTGAGT GGATGGGAAA  
TATCATCCCT GTCTATAATA CACCAAACTA CGGCAGAAAG TTTCAGGGA GACTCTCGAT AACCGCCGAC  
GATTCACGA GCACAGCCTA CATGGAACCTG AGTAGCCTCA GATCTGAGGA CACGGCCGTC TATTTCTGTG  
CGAGAGTCGT AATACCAAAT GCAATCCGGC ACACGATGGG ATATTACTTT GACTACTGGG GCCAGGGAAC  
CCTGGTCACC GTCTCCTCA

(1:7, HEAVY CHAIN) [SEQ ID NO.: 23]

## FIG. 4B



## FIG. 4C

(1:11, HEAVY CHAIN) [SEQ ID NO.: 24]

CTCGAGCAGT CTGGGGCTGA GGTGAAGAAG CCTGGGTCCT CAGTGAAGGT CTCCTGCAAG GCTTCTGGAG  
GCACCTTCAG CGGCCATGTT ATCAGCTGGG TGCACAGGC CCTGGACAA GGCCTTGAGT GGATGGGGG  
GAGTATCTCT TTCTTTGGCA CATCAAACTC CGCACAGAAG TTCCAGGGCA GAGTCTCGAT TACCGGGGAC  
GAATCCGCGA GCACAGCCTA CATGGAGCTG AGTAGCCTGA GATCGGAGGA CACGGCCATC TATTACTGTG  
CGAAGAGCCC TCCAAGATTT TGTAGTGGTG GTAACCTGCTA CCCGGGGTTC TTCCAGCAGT GGGGCCAGGG  
CACCTGGTC ACCGTCTCCT CA

## FIG. 4D

(1:3, HEAVY CHAIN) [SEQ ID NO.: 25]

CTCGAGTCGG GGGAGGGCGT GGTCCAGCCT GGGAGGTCCC TGAGACTCTC CTGTGCAGCG TCTGGATTCA  
CCTTCAAGAC GTATGGCATG CACTGGGTCC GCCAGGCTCC AGGCAAGGG CTGGAGTGGG TGGCAGGTAT  
TTCGTTTGAT GGAAGTAACC AATATTACGC AGACTCCGTG AAGGGCCGAT TCATCGTCTC CAGAGACAAT  
TCCAGGGACA CGGTGTTTCT GCAGATGAGC AGCCTGAGAC TCGAGGACAC GGCTGTCTAT TACTGTGCGA  
CAGAGGGTTC TCCTTTTGGC TCGATTAAAG GGC GTTACTA CCTTGAAAT TGGGGCCAGG GAACCTGGT  
CACCGTCTCC TCA



FIGURE 4E (L1, HEAVY CHAIN) [SEQ ID NO.: 19]

GAGGTGCAGC TGCTCGAGTC TGGGGGAGGC GTGGTCCAGC CTGGGAGGTC CCTGAGACTC TCCTGTGCAG  
CGTCTGGATT CACCTTCAGT GCTTATGGCA TGCACCTGGT CCGCCAGGCT CCAGGCAAGG GGCTGGAGTG  
GGTGGCAGGT ATATGGTTTG ATGGAAGTAA TCAATACTAT TCAGACTCCG TGAAGGGCCG ATTCAACCGTC  
TCCAGAGACA ATCCAGGAA CACGCTGTTT CTGCAAAATGA ACAGCCTGAG ACCCGAGGAC ACGGCTGTCT  
ATTACTGTGC GACAGAGGTA CTTTTTGGAT CGATTAGGG GCGTTACTAC CTTGAAAACT GGGGCCAGGG  
AACCCTGGTC ACGTCTCCT CA

FIGURE 4F (A8, HEAVY CHAIN) [SEQ ID NO.: 26]

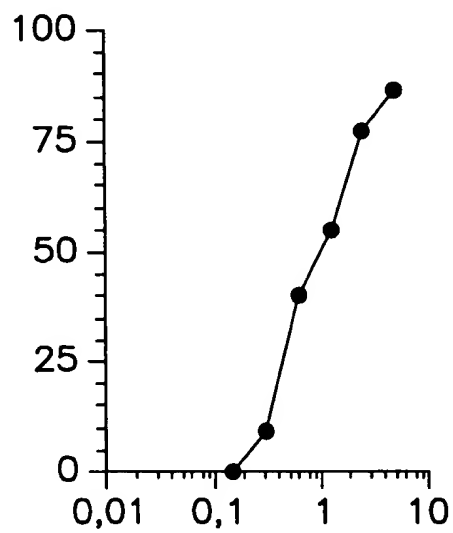
GAGGTGCAGC TGCTCGAGTC GGGCCCAGGA CTGGTGAAGC CTTGGGGGAC CCTGTCCCTC ACCTGCACCTG  
TCTCTGGTGG CTCCATCAGG AGCAGTCACT GGTGGAGTTG GGTCCGCCAG CCCCCAGGA AGGACTGGA  
GTGGATTGGA GAAGTCTTTT TTAGTGGAAG CACCATCTAC AACCCTATCC TCAACGATCG AGTCTTCATG  
TCTGTAGACA AGTCCAAGGA CCAGGTCCTCC CTGAGGCTGA GCTCTGTGAC CGCCGCGGAC ACGGCCGTGT  
ATTACTGTGC GAGATCCCTC ATAAAATGA ATCAGGGAAG ATGATGTTG GATGCTTTG ATATCTGGGG  
CCAGGGGACA CTCGTCATCG TCTCTTCC

FIGURE 4G (A12, HEAVY CHAIN) [SEQ ID NO.: 27]

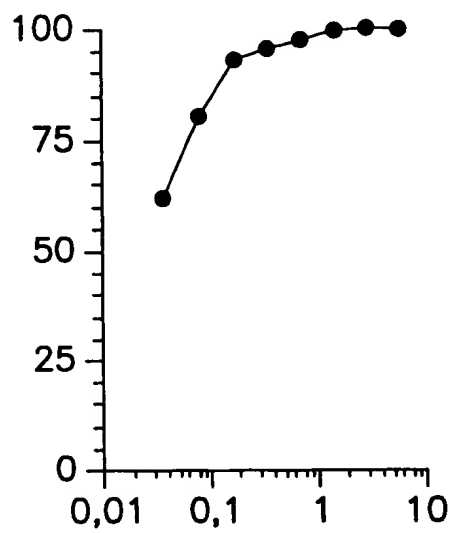
GAGGTGCAGC TGCTCGAGTC TGGGTCTGAG GTGAAGAAGC CTGGGTCTTC GGTGAAGGTC TCCTGCAGGG  
CCTCTGGAGG CAGCTTCAGA AGCTACAATT TCAATTGGGT GCGACAGGCC CCTGGACAAG GTCTTGAGTG  
GATGGGAGGC ATCATCCCTA TGTTCGGAAC AGCAAACTAC GCACAGAAGT TTCAGGGCAG AGTCACAATT  
ACCGGGGACG AATCCACGGC CACAGGCTAC ATGGAGTTGA GCAGTCTGAG ATCTGAAGAC ACGGCCGTTT  
ATTACTGTGC GATGCCCTAT CCAAAACATT GCAGTCGTGG AAGTGTCTGG GGCTGGITCG ACCCCTGGGG  
CCAGGGAACCT CTGGTCACCG TGTCTTCA



% Neutralisation of E2 (HCV-1a) binding



L3



1:5

Monovalent Fab [ g/ml]

1:7

FIG. 5

1:11